SEQUENCE LISTING

(1) GENERAL INFORMATION: (i) APPLICANT: SCHENDEL, Dolores J. (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA (iii) NUMBER OF SEQUENCES: 44 (iv) CORRESPONDENCE ADDRESS: ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP (A) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby (B) (C) CITY: Washington (D) STATE: DC (E) COUNTRY: USA (F) ZIP: 20005-5701 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/Mg-DOS (C) (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (vi) CURRENT APPLICATION DATA: APPLICATION NUMBER: 08/881,509 (A) FILING DATE: June 24/1997 (B) (C) CLASSIFICATION: (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Kitts, Monica Chin (B) REGISTRATION NUMBER: 36,105 (C) REFERENCE/DOCKET NUMBER: 564-7015 (ix) TELECOMMUNICATION INFÓRMATION: (A) TELEPHONE: (202) 638-5000 TELEFAX: (202) 638-4810 (B) (2) INFORMATION FOR SEQ ID NO: 1: (i) SEQUENCE CHARACTERISTICS: LENGTH: 1341 base pairs (A) TYPE: nucleic acid (B) (C) STRANDEDNESS: both (D) TOFOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..801 FFATURE: (A) NAME/KEY: sig_peptide (B)LOCATION: 1..54

FEATURE:

NAME/KEY: mat peptide

(B) LOCATION:55..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

### ATG AGG CAA GTG GCG AGA GTG ATC GTG ATC CTG ACC CTG AGT ACT TTG ### ATG GIN Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu -18			,	,	_	-20	21101		DCIVE	- 110	IN: S	₽Õ I	וו ט	o:	1:							
CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT GIN Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 30 25 30 30 30 25 30 30 30 30 30 30 30 30 30 30 30 30 30				G C		Val	GC0 Ala	G AG	A GTO	G ATO	e va	T 5P	C C	TG . eu	ACC Thr	CT(ي Se	r Th	T T	TG eu		48
TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT TYP Ile Thr Trp Tyr Gin Gin Phe Pro Ser Gin Giy Pro Arg Phe Ile 35 ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG CCC CTG TTT Ile Gin Giy Tyr Lys Thr Lys Val Thr Asn Giu Val Ala Ser Leu Phe 50 ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCC GAG AGC AGC AGC ACT CTG AGC GGT GTT TT ATC ACT GGT GTG AGC ACT GTG TTT TACT GAT ATC GGIn Leu Thr Phe Gly Ser Gly Thr Gin Leu Thr Val Leu Pro Asp Ile 100 CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gin Leu Thr Phe Gly Ser Gly Thr Gin Leu Thr Val Leu Pro Asp Ile 100 CAG AAC CCT GAC CCT GCC GTG FAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gin Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 GAC AAG ACG TCT ATG GAC TTT GAA AGC AAC GTG GCT GTG GCC TGG AGC ASP Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAA ACC GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AAC GCC TGA ASP Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GAC AAC Pro Glu Asp Thr Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys TTT TTT TTT TTT TTT TTT TTT TTT TTT T		AG0 Sei	C CT	T GO	.u.	AAG Lys	ACC Thr	C AC	r. GTI	1 Pro	C ATO	C TC e Se	C A' r M	IG (Asp	Sei	A/TA Ty	T GA r Gl	A Go u G	GA ly		96
ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT Ile Gln Gly Tyr Lys Thr Lys Val Thr Asa Glu Val Ala Ser Leu Phe 50 ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGG CTG CGC CGG GTT TCC 11e Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT GCT AGG CGC AGG GTT TCC 11e Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg 80 CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 100 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 GAC AAG TCT GTC TGC CTA T/C ACC GAT TTT GAT TCT CAA ACA AAT GTG ASp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 155 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC ASP Met Arg Ser Met Asp Phe Lys Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 155 GAC ATG AGG TCT ATG GAC TTC CAA AGC AAC AGT GCT GTG GCC TGG AGC ASP Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC CAA ACT AGC ATT GAC TTC CAA ACC GAT TTC AAC AAC AAC ACT ATT ATC ACA AAC AAC			. 01	A GT u Va	TG A	AAC Asn	ATA	: T111	- Cys	AGC Ser	C CAC	C AA s As	n As	sn I	ATT	GCT Ala	AC.	A AA r As	n As	sp		144
ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC ILle Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GCT GCT CGC AGG GTT TCC 165 CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GCT GCT TCT GCA AGG 165 CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC 160 Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ille 165 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT 110 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT 110 CAG AAC CCT GAC CCT GCC GTG TAC CAC GTG AGA GAC TCT AAA TCC AGT 110 CAG AAC TCT GTC TCC CTA TCC ACC GAT TTT GAT TCT CAA ACA AAT GTG ASp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 135 TCA CAA AGT AGG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 150 GAC ATG AGG TCT ATG ACC TTC AAG ACC AAC AGT GCT GTG GCC TGG AGC ASP Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 165 AAC AAA TCT GAC TT GCA TGT GCA AAC GCC TTC AAC ACA AAC AGC ATT ATT ASN Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 185 CCA GAA GAC ACC TTC TCC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG ACC ATT ATT ASN Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 185 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG ACC ACC ATT ATT ASN Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 190 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG ACC ACC ACC ACC ACC ACC ACC ACC AC		TAT Tyr	ATO	C AC	G] ir]	rgg rp	TÄT	GII	A CAG	TTI Phe	CCC Pro	se:	r G1	AA (/ SGA Sly	CCA Pro	CG Are	g Ph	e Il	TT Le		192
CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg 80 CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 100 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 GAC AAG TCT GTC TGC CTA TrC ACC GAT TTT GAT TCT CAA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 180 CCA GAA GAC ACC CTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 672		ATT	Gl:	A GG n Gl	АТ	ΥΫ́	AAG Lys	ACA Thr	AAA Lys	GTT Val	Thr	: Ası	C GA	/ A ∈ u V	IG /al	GCC A)a	Sei	Lei	G TT ı Ph	T ie		240
CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 100 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC ACT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 180 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 672		ATC Ile	CCT Pro		u 23	SAC sp	AGA Arg	AAG Lys	TCC Ser	ser	ACT Thr	CTO	AG Se	r/L	CTG Leu	CCC Pro 75	CG0 Arc	GTT J Val	T TC	C		288
CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT GIN Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 125 GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 155 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT ASh Lys Ser Asp Phe Ala Cys Ala Ash Ala Phe Ash Ash Ser Ile Ile 185 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG ACC Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG ACC Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys A32 Leu Pro Asp Ile 110 110 Leu Pro Asp Ile Pro Asp Ile Ile 110 120 432 432 432 432 432 432 432 4		CTG Leu	001	ns,	C A p T	CT hr	GCT Ala	GTG Val	Tyr	TAC Tyr	TGC Cys	CTC Leu	GT Va	l G	ly	GT Sly	TCI Ser	GCA	AG Ar	G g		336
GAC AAG TCT GTC TGC CTA TCT ACC GAT TTT GAT TCT CAA ACA AAT GTG ASP Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 155 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 165 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 185 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Cys Asp Val Lys GAC AAG TCT GAC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys		0111	CTG Leu	ACC Th:	C T'	TT (GGA Gly	ser	GGG Gly	ACA/ Tha	CAA Gln	TTG Leu	Th.	r V	TT/al	TTA Leu	CCT Pro	GAT Asp	Il	е		384
TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 672	ı	CAG Gln	AAC Asn	CC: Pro	r G	sb 1	LTO	GCC Ala	GTG Val	TAC Tyr	CAG Gln	Leu	Ar	A G	AC sp	TCT Ser	AAA Lys	Ser	AG' Sei	ľ		432
GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys GAC TTG AAG AGC TTG AAG AGC AGC AAC AGC AGC ATT ATT ASD Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 180 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG AGA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG	í	GAC Asp	AAG Lys	TCT Ser		aT (rgc Cys	CTA Leu	T/TC Phe	ACC Thr	Asp	TTT Phe	GA: Asp	΄ Τ(> Se	CT er	CAA Gln	Thr	AAT Asn	GT(Va)	3 L		480
AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 180 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 624 672		rca Ser	CAA Gln			AG G /s <i>P</i>	SAT Asp	TCT Ser	GAT Asp	Val	TAT Tyr	ATC Ile	ACA Thr	A GA	sp]	Lys	ACT Thr	GTG Val	CT <i>F</i> Let	A 1		528
CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 672	Į	GAC Asp	11C C	AGG Arg	TC	er M	TG let	GAC Asp	Pne	AAG Lys	AGC Ser	AAC Asn	AGI Ser	Al	a V	GTG Val	GCC Ala	TGG Trp	AGC Ser			576
In the File Fro Ser Pro Glu Ser Ser Cys Asp Val Lys	-		AAA Lys	TCT Ser	GA As	C T	$\mu \in I$	нта	TGT Cys	GCA . Ala .	AAC Asn	GCC Ala	Phe	AA As	AC F	AAC . Asn .	AGC Ser	ATT Ile	Ile			624
1	P	CA Pro	GAA Glu	GAC Asp	AC Th	- /-	116 1	TTC Phe	CCC . Pro :	AGC (Ser)	Pro	Glu	AGT Ser	TC Se	C I	TGT (Cys)	GAT Asp	Val	AAG Lys			672

CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gin Asn 210 215	720
CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GGC GGG TTT Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe 225 235	768
AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser 240 245	821
GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG	881
AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA	941
ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA	1001
CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA	1061
GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGGTCCC CAGAGACTGC	1121
CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGGTCTA GGTCCTGGAG	1181
AATGTTGTGA GGGGTTTATT TTTTTTTAAT ACTGTTCATA AAGAAATACA TAGTATTCTT	1241
CTTCTCAAGA CGTGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG	1301
GGCGTGTTGT ATGTCCTGCT GCCGATGCCT TCATTAAAAT	1341
(2) INFORMATION FOR SEQ ID NO: 2:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	٠
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu -18 -15 -5	
Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly 1 5 10	
Gln Glu Val Asn/Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 20 25 30	
Tyr Ile Thr Typ Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile 35 40 45	
Ile Gln Gly fyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe 50 60	
Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser	

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg

Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 95 100 105 110

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Ash Ser Ile Ile 175 180 185 190

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 210

Leu Ser Val Ile Gly Phe Arg Ide Leu Leu Leu Lys Val Ala Gly Phe

Asn Leu Leu Met Thr Leu Ard Leu Trp Ser Ser 240

(2) INFORMATION FOR SEQ/ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE:/nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LØCATION:1..933
 - (ix) FEAT/URE:
 - (A) /NAME/KEY: sig_peptide
 - (B) $\int LOCATION: 1...6\overline{3}$
 - (ix) FEATURE:
 - (A)/ NAME/KEY: mat_peptide
 - (B) LOCATION: $64..\overline{9}33$
 - (xi) /SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala -21 -20

48

GGA Gly	у до	C AC	A GAA	A CC	O GI	A GTO u Va. 1	C AC	C CA	G AC n Th	T CC r Pr 5	C AG	GC CA	AT C	ln/Vá	/ CC ACA il Thi	<i>A</i>	96
CA(Glr	G ATO	G GGZ	A CAC y Glr 15	1 GT	A GTO	G ATO	C TT(e Let	G CGG 1 Arg 20	д Су:	T GT s Va	C CC l Pr	C AT	.e/ S	CT AF er As 25	T CAC	3	144
TTA Leu	A TAC	TT(Phe 30	- TAT	TGC Trp	TAC Ty	C AGA	A CAA g Glr 35	j TT€	C TTO	G GG u Gl	G CA y Gl	n/ Ly	A G' s Va 0	rc ga al gl	G TTT u Phe	•	192
CTG Leu	GTT Val 45	. ser	C TTT Phe	TAT Tyr	AA1 Asr	TAA T Asr 50	ı GIt	ATO	C TCA e Sei	A GA	G AA u Ly 5	s Se	T GA r Gl	AA AT u Il	A TTC e Phe		240
GAT Asp 60	ASP	CAA Gln	TTC Phe	TCA Ser	GTT Val	. GIU	AGG Arg	CCT Pro	GAT Asp	G1:	y Se:	A AA As:	T) TI	C AC e Th	T CTG r Leu 75		288
AAG Lys	ATC Ile	CGG Arg	TCC Ser	ACA Thr 80	гуу	CTG Leu	GAG Glu	GAC Asp	C/ICA Ser 85	Ala	C ATO	G TAC	TT Ph	C TG e Cy	F GCC S Ala		336
AGC Ser	AGC Ser	GAA Glu	ACT Thr 95	AAC Asn	TCC Ser	TAC Tyr	GAG Glu	ÇAG Gln 100	Tyr	TTC Phe	GG(Gl _y	G CCC	G GG O G1 10	y Thi	C AGG Arg		384
CTC Leu	ACG Thr	GTC Val 110	ACA Thr	GAG Glu	GAC Asp	CTG Leu	AAA Lys 115	AAC Asn	GTG Val	TTC Phe	CCF Pro	CCC Pro 120	Gl	G GT(u Val	C GCT Ala		432
GTG Val	TTT Phe 125	GAG Glu	CCA Pro	TCA Ser	GAA Glu	GOA Ala 130	GAG Glu	ATC Ile	TCC Ser	CAC His	ACC Thr 135	Glr	AA	G GCC s Ala	ACA Thr		480
CTG Leu 140	GTG Val	TGC Cys	CTG Leu	GCC Ala	ACA Thr 145	GGC Gly	TTC Phe	TAC Tyr	CCC Pro	GAC Asp 150	CAC His	GTG Val	GA(Gl)	G CTG 1 Leu	AGC Ser 155		528
TGG Trp	TGG Trp	GTG Val	AAT Asn	GGG Gly 160	AAG Lys	GAG Glu	GTG Val	CAC His	AGT Ser 165	GGG Gly	GTC Val	AGC Ser	AC? Thi	A GAC Asp 170	Pro		576
CAG Gln	CCC Pro	CTC Leu	AAG Lys 175/	GAG Glu	CAG Gln	CCC Pro	GCC Ala	CTC Leu 180	AAT Asn	GAC Asp	TCC Ser	AGA Arg	TAC Tyr 185	TGC Cys	CTG Leu		624
AGC Ser	Der	CGC Arg 190	CTG L∉u	AGG Arg	GTC Val	Ser	GCC Ala 195	ACC Thr	TTC Phe	TGG Trp	CAG Gln	AAC Asn 200	CCC	CGC Arg	AAC Asn		672
	TTC Phe 205	CGC Arg/	TGT Cys	CAA Gln	GTC Val	CAG Gln 210	TTC Phe	TAC Tyr	GGG Gly	CTC Leu	TCG Ser 215	GAG Glu	AAT Asn	GAC Asp	GAG Glu		720
TGG 7 Trp 220	ACC (Thr	CAG Gln.	GAT A	arg.	GCC Ala 225	AAA Lys	CCT Pro	GTC Val	Thr	CAG Gln 230	ATC Ile	GTC Val	AGC Ser	GCC Ala	GAG Glu 235		768

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GCC Ala	TGG Trp	GGT Gly	AGA Arg	GCA Ala 240	a Asj	C TG! p Cys	r GG0 s Gly	C TTO y Phe	C ACc e Th: 24:	r Se	C GA r Gl	G TC u Se	T TA r Ty	C CA r G1: 25	G ØAA n Gln		816
GGG Gly	GTC Val	CTG Leu	TCT Ser 255	ATS	C ACC	C AT(C CTO	TA: 1 Ty: 260	r GI	G AT u Il	C TT e Le	G CT. u Le	A GG u G1: 26	y Ly	G GCC s Ala		864
ACC Thr	TTG Leu	TAT Tyr 270	GCC Ala	GTG Val	CT(G GT(ı Val	AGT Ser 275	: Ala	C CTO	C GT	G CTO	G AT(u Me) 28(G/GCG Ala	C ATO	G GTC Val		912
Lys	AGA Arg 285	AAG Lys	GAT Asp	TCC Ser	AGA Arg	A GGC g Gly 290	•	3				/	$\overline{}$				936
(2)	TNFC	ימאמי	rt (N	EOD	C E C	\ TD	NO.	4		/							
	INE) ID					/						
(i)		SEÇ (A)				CTER 311			ids				/				
		(B) (D)	. 1	ΓΥΡΕ	: am	ino : li	acid			`			/				
	(ii					E: p											
	(xi																
34 . (CRIP		/				/					
Met 2 -21	-20	Thr	Trp	Leu	Val	Cys -15	Trr	Ala	Ile	Phe	Ser -10	Leu	Leu	Lys	Ala		
Gly 1 -5	Leu	Thr	Glu	Pro	Glu 1	Val	Thr	Gln	Thr 5	Pro	Ser	His	Gln	Val 10			
Gln N	Met	Gly	Gln 15	Glu	Val	IZe	Leu	Arg 20	Cys	Val	Pro	Ile	Ser 25	Asn	His		
Leu 1	ſyr	Phe 30	Tyr	Trp	Тут	Arg	Gln 35	Ile	Leu	Gly	Gln	Lys 40	Val	Glu	Phe		
Leu V	/al : 45	Ser	Phe	Tyr	Asn	Asn 50	Glu	Ile	Ser	Glu	Lys 55	Ser	Glu	Ile	Phe		
Asp A	lsp (Gln :	Phe	Ser	Val 65	Glu	Arg	Pro	Asp	Gly 70	Ser	Asn	Phe	Thr	Leu 75		
Lys I	le A	Arg :	Ser/	Thr 80	Lys	Leu	Glu	Asp	Ser 85	Ala	Met	Tyr	Phe	Cys 90	Ala		
Ser S	er (Glu :	7%r 1 95	Asn	Ser	Tyr	Glu	Gln 100	Tyr	Phe	Gly	Pro	Gly 105	Thr	Arg		
Leu T	-	/al/1	Chr (Glu	Asp	Leu	Lys 115	Asn	Val	Phe	Pro	Pro 120	Glu	Val	Ala		
Val P	he 6 25	S/u E	Pro S	Ser	Glu	Ala 130	Glu	Ile	Ser	His	Thr 135	Gln	Lys	Ala	Thr		
Leu V	al	Cys I	⊾eu A	Ala '	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser		

140

145

150

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu 180

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn/Pro Arg Asn

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Clu Asn Asp Glu

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln The Val Ser Ala Glu 230

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Gly Ser Tyr Gln Gln 240

Gly Val Leu Ser Ala Thr Ile Leu Tyr/G/u Ile Leu Gly Lys Ala 255 260

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val 275 280

Lys Arg Lys Asp Ser Arg Gly

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- LENGTH: 39 base pairs (A)
- TYPE: nugleic acid (B)
- (C)
- STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- LOCATION:1..39 (B)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC CTC GTC CTT/TCT GGT TCT GCA AGG CAA CTG ACC TTT Cys Leu Val Ley Ser Gly Ser Ala Arg Gln Leu Thr Phe 295

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- LENGTH: 13 amino acids
- (B) TYPE: amino acid
- TOPOLOGY: linear (D)
- (i‡)
- SEQUENCE DESCRIPTION: SEQ ID NO: 6:

39

MOLECULE TYPE: protein

Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: LENGTH: 36 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..36 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: TGC CTC GCT ACT GGT TCT GCA AGG CAA CTG/ACC TTT Cys Leu Ala Thr Gly Ser Ala Arg Gln/Lex Thr Phe 20 (2) INFORMATION FOR SEQ ID NO: 8: (i)SEQUENCE CHARACTERISTICS: LENGTH: 12 amino/acids (A) (B) TYPE: amino aciá (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe (2) INFORMATION FOR ≸EQ ID NO: 9: (i) SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs (A) TYPE: nucleic acid (B) (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..39

39

36

(2) INFORMATION FOR SEQ ID NO: 10:

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGT GCC AG ϕ AGT GGA ACA GAT TCC TAC GAG CAG TAC TTC Cys Ala Se ϕ r Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe

(xi)

TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe

- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:

(D)

- (A) NAME/KEY: CDS
- (B) LOCATION:1..39
- (xi) SEQUENCE DESCRIPTION: EQ ID NO: /11:

TGT GCC AGC AGT GAA ACA GAT TCC/TAC GAG CAG TAC TTC
Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gin Tyr Phe
15 20 25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE/DESCRIPTION: SEQ ID NO: 12:

Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe
1 10

(2) INFORMATION/FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) / LENGTH: 39 base pairs
 - (B) / TYPE: nucleic acid
 - (C) / STRANDEDNESS: both
 - (D)/ TOPOLOGY: linear
 - (ix) /FEATURE:
 - (♣) NAME/KEY: CDS
 - (B) LOCATION:1..39

39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: TGT GCC AGC AGT GGA ACA GCT TCC TAC GAG CAG TAC TTC 39 Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe (2) INFORMATION FOR SEQ ID NO: 14: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 14: Cys Ala Ser Ser Gly Thr Ala Ser Tyr Gly Gln Tyr Phe (2) INFORMATION FOR SEQ ID NO: 15 (i) SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: Noth (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: QDS (B) LOCATION: 1..39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: TGT GCC AGC AGT GGT ACA AAC TCC TAC GAG CAG TAC TTT 39 Cys Ala Ser Ser Gly 7hr Asn Ser Tyr Glu Gln Tyr Phe (2) INFORMATION FOR SEQ ID NO: 16: (i) SEQUENCÉ CHARACTERISTICS: ZENGTH: 13 amino acids (A) (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16: Cys Ala Se η' Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe 1 (2) INFORMATION FOR SEQ ID NO: 17:

(i)

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1...39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: TGT GCC ACC TCC GGG ACA GCT TCC TAC GAG CAG TAC TTC 39 Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe 20 (2) INFORMATION FOR SEQ ID NO: 18: (i) SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids (A) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: ≸EQ ID NO: 18: Cys Ala Thr Ser Gly Thr Ala Ser/Tyr Glu Gln Tyr/Phe (2) INFORMATION FOR SEQ ID NØ: 19: (i) SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS LOCATION:1..39 (B) (xi) SEQUENCE/DESCRIPTION: SEQ ID NO: 19: TGT GCC AGA TCC GG ACA GGC TCC TAC GAG CAG TAC TTC 39 Cys Ala Arg Ser G#y Thr Gly Ser Tyr Glu Gln Tyr Phe 15 20 (2) INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe
 (2) INFORMATION FOR SEQ ID NO: 21:
 (i)
          SEQUENCE CHARACTERISTICS:
           (A)
                LENGTH: 20 base pairs
           (B)
                TYPE: nucleic acid
          (C)
                STRANDEDNESS: single
          (D)
                TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:
 CACTGAAGAT CCATCATCTG
                                                                              20
 (2) INFORMATION FOR SEQ ID NO: 22:
 (i)
          SEQUENCE CHARACTERISTICS:
          (A)
                LENGTH: 20 base pairs
          (B)
                TYPE: nucleic acid
          (C)
                STRANDEDNESS: single
          (D)
                TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: /SEQ ID NO: 22:
TAGAGGATGG TGGCAGACAG
                                                                              20
(2) INFORMATION FOR SEQ ID NO:23:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 Amino acids
          (B) TYPE: aming acid
          (C) STRANDEDNES: not relevant
          (D) TOPOLOGY: / not relevant
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 4..8
          (C) OTHE INFORMATION: /note= "Xaa(1) to Xaa(5) represents a
sequence of 3 to \beta amino acids
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
    Tyr Cys Leu Xaa Xaa Xaa Xaa Ser Ala Arg Gln Leu Thr Phe
(2) INFORMATION FOR SEQ ID NO:24:
    (i) SE⊄UENCE CHARACTERISTICS:
          (A) LENGTH: 14 amino acids

√B) TYPE: amino acid
```

- (C) STRANDEDNESS: not relevant(D) TOPOLOGY: not relevant(ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gla Gln Tyr Phe

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asn Glu Gln Phe Phe

- (2) INFORMATION FOR SEQ/ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH; 14 amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE/TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5/to 7 amino acids
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Gln Tyr Phe

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Ser Glu Thr Asn Ser 1 5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION SEQ ID NO:28:

Ser Ser Glu Thr Ser Ser 1

(2) INFORMATION FOR SEQ /ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: /6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLÓGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Thr Ala Ser

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (Å) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Ser Gly Thr Gly Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

Ser Ser Gly Thr Asp Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not ≠elevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: pepti**⊄**e
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Ser Gly Thr Arg Ser

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH / 6 amino acids
 - (B) TYPE: /amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUEN DESCRIPTION: SEQ ID NO:33:

Ser Ser Gly Ser Asp Ser

- (2) INFORMAT ON FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - IB) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Ser Ser Thr Gly Ser

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ /D NO:35/:

Ser Ser Ser Thr Val Ser

- (2) INFORMATION FOR SEQ ID NO /36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 ami/no acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: Not relevant /
 - (ii) MOLECULE TYPE/ peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Ser Thr Leu Ser

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) /TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D/ TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Ser Ser Thr Leu Phe 1

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Ser Thr Ala Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant.
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser His Thr Asp Ser 1 5

- (2) INFORMATION FOR SEQ ID/NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6/amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE/DESCRIPTION: SEQ ID NO:40:

Ser Ser Asp Thr Leu Ser 1

- (2) INFORMAT ON FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii ∕ MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Arg Trp Asp Ser Glu
1 5

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ser Ser Gly Thr Ser Ser Tyr 5

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ser Asp Gln Gly Met

- (2) INFORMATION FOR SEØ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ala Asp Ser Phe Lys